

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 09/825,212A  
Source: IFW/6  
Date Processed by STIC: 3/22/05

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 03/22/2005

PATENT APPLICATION: US/09/825,212A

TIME: 11:46:19

Input Set : A:\Seq.Listing.txt

Output Set: N:\CRF4\03222005\I825212A.raw

3 &lt;110&gt; APPLICANT: Benson, Timothy E.

5 &lt;120&gt; TITLE OF INVENTION: CRYSTALLIZATION AND STRUCTURE DETERMINATION OF STAPHYLOCOCCUS

6 AUREUS THIOREDOXIN REDUCTASE

8 &lt;130&gt; FILE REFERENCE: 0032.US1

10 &lt;140&gt; CURRENT APPLICATION NUMBER: 09/825,212A

11 &lt;141&gt; CURRENT FILING DATE: 2001-04-03

13 &lt;150&gt; PRIOR APPLICATION NUMBER: US 60/195,055

14 &lt;151&gt; PRIOR FILING DATE: 2000-04-06

16 &lt;160&gt; NUMBER OF SEQ ID NOS: 3

18 &lt;170&gt; SOFTWARE: PatentIn version 3.2

20 &lt;210&gt; SEQ ID NO: 1

21 &lt;211&gt; LENGTH: 320

22 &lt;212&gt; TYPE: PRT

23 &lt;213&gt; ORGANISM: staphylococcus aureus

25 &lt;400&gt; SEQUENCE: 1

27 Met Gly Thr Glu Ile Asp Phe Asp Ile Ala Ile Ile Gly Ala Gly Pro

28 1 5 10 15

31 Ala Gly Met Thr Ala Ala Val Tyr Ala Ser Arg Ala Asn Leu Lys Thr

32 20 25 30

35 Val Met Ile Glu Arg Gly Ile Pro Gly Gly Gln Met Ala Asn Thr Glu

36 35 40 45

39 Glu Val Glu Asn Phe Pro Gly Phe Glu Met Ile Thr Gly Pro Asp Leu

40 50 55 60

43 Ser Thr Lys Met Phe Glu His Ala Lys Lys Phe Gly Ala Val Tyr Gln

44 65 70 75 80

47 Tyr Gly Asp Ile Lys Ser Val Glu Asp Lys Gly Glu Tyr Lys Val Ile

48 85 90 95

51 Asn Phe Gly Asn Lys Glu Leu Thr Ala Lys Ala Val Ile Ile Ala Thr

52 100 105 110

55 Gly Ala Glu Tyr Lys Lys Ile Gly Val Pro Gly Glu Gln Glu Leu Gly

56 115 120 125

59 Gly Arg Gly Val Ser Tyr Cys Ala Val Cys Asp Gly Ala Phe Phe Lys

60 130 135 140

63 Asn Lys Arg Leu Phe Val Ile Gly Gly Gly Asp Ser Ala Val Glu Glu

64 145 150 155 160

67 Gly Thr Phe Leu Thr Lys Phe Ala Asp Lys Val Thr Ile Val His Arg

68 165 170 175

71 Arg Asp Glu Leu Arg Ala Gln Arg Ile Leu Gln Asp Arg Ala Phe Lys

72 180 185 190

75 Asn Asp Lys Ile Asp Phe Ile Trp Ser His Thr Leu Lys Ser Ile Asn

76 195 200 205

79 Glu Lys Asp Gly Lys Val Gly Ser Val Thr Leu Thr Ser Thr Lys Asp

80 210 215 220

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83 Gly Ser Glu Glu Thr His Glu Ala Asp Gly Val Phe Ile Tyr Ile Gly
84 225                230                235                240
87 Met Lys Pro Leu Thr Ala Pro Phe Lys Asp Leu Gly Ile Thr Asn Asp
88                245                250                255
91 Val Gly Tyr Ile Val Thr Lys Asp Asp Met Thr Thr Ser Val Pro Gly
92                260                265                270
95 Ile Phe Ala Ala Gly Asp Val Arg Asp Lys Gly Leu Arg Gln Ile Val
96                275                280                285
99 Thr Ala Thr Gly Asp Gly Ser Ile Ala Ala Gln Ser Ala Ala Glu Tyr
100                290                295                300
103 Ile Glu His Leu Asn Asp Gln Ala Arg Ser His His His His His
104 305                310                315                320
107 <210> SEQ ID NO: 2
108 <211> LENGTH: 320
109 <212> TYPE: PRT
110 <213> ORGANISM: escherichia coli
112 <400> SEQUENCE: 2
114 Gly Thr Thr Lys His Ser Lys Leu Leu Ile Leu Gly Ser Gly Pro Ala
115 1                5                10                15
118 Gly Tyr Thr Ala Ala Val Tyr Ala Ala Arg Ala Asn Leu Gln Pro Val
119                20                25                30
122 Leu Ile Thr Gly Met Glu Lys Gly Gly Gln Leu Thr Thr Thr Thr Glu
123                35                40                45
126 Val Glu Asn Trp Pro Gly Asp Pro Asn Asp Leu Thr Gly Pro Leu Leu
127                50                55                60
130 Met Glu Arg Met His Glu His Ala Thr Lys Phe Glu Thr Glu Ile Ile
131 65                70                75                80
134 Phe Asp His Ile Asn Lys Val Asp Leu Gln Asn Arg Pro Phe Arg Leu
135                85                90                95
138 Asn Gly Asp Asn Gly Glu Tyr Thr Cys Asp Ala Leu Ile Ile Ala Thr
139                100               105               110
142 Gly Ala Ser Ala Arg Tyr Leu Gly Leu Pro Ser Glu Glu Ala Phe Lys
143                115               120               125
146 Gly Arg Gly Val Ser Ala Cys Ala Thr Cys Asp Gly Phe Phe Tyr Arg
147                130               135               140
150 Asn Gln Lys Val Ala Val Ile Gly Gly Gly Asn Thr Ala Val Glu Glu
151 145               150               155               160
154 Ala Leu Tyr Leu Ser Asn Ile Ala Ser Glu Val His Leu Ile His Arg
155                165                170                175
158 Arg Asp Gly Phe Arg Ala Glu Lys Ile Leu Ile Lys Arg Leu Met Asp
159                180                185                190
162 Lys Val Glu Asn Gly Asn Ile Ile Leu His Thr Asn Arg Thr Thr Glu
163                195                200                205
166 Glu Val Thr Gly Asp Gln Met Gly Val Thr Gly Val Arg Leu Arg Asp
167                210                215                220
170 Thr Gln Asn Ser Asp Asn Ile Glu Ser Leu Asp Val Ala Gly Leu Phe
171 225                230                235                240
174 Val Ala Ile Gly His Ser Pro Asn Thr Ala Ile Phe Glu Gly Gln Leu
175                245                250                255

```

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178 Glu Leu Glu Asn Gly Tyr Ile Lys Val Gln Ser Gly Ile His Gly Asn
179          260          265          270
182 Ala Thr Gln Thr Ser Ile Pro Gly Val Phe Ala Ala Gly Asp Val Met
183          275          280          285
186 Asp His Ile Tyr Arg Gln Ala Ile Thr Ser Ala Gly Thr Gly Cys Met
187          290          295          300
190 Ala Ala Leu Asp Ala Glu Arg Tyr Leu Asp Gly Leu Ala Asp Ala Lys
191 305          310          315          320
194 <210> SEQ ID NO: 3
195 <211> LENGTH: 333
196 <212> TYPE: PRT
197 <213> ORGANISM: Arabidopsis thaliana
199 <400> SEQUENCE: 3
201 Met Asn Gly Leu Glu Thr His Asn Thr Arg Leu Cys Ile Val Gly Ser
202 1          5          10          15
205 Gly Pro Ala Ala His Thr Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu
206          20          25          30
209 Lys Pro Leu Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly
210          35          40          45
213 Gly Gln Leu Thr Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Pro
214          50          55          60
217 Glu Gly Ile Leu Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser
218 65          70          75          80
221 Glu Arg Phe Gly Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp
222          85          90          95
225 Phe Ser Ser Lys Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu
226          100         105         110
229 Ala Asp Ala Val Ile Leu Ala Ile Gly Ala Val Ala Lys Arg Leu Ser
230          115         120         125
233 Phe Val Gly Ser Gly Glu Val Leu Gly Gly Phe Trp Asn Arg Gly Ile
234          130         135         140
237 Ser Ala Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys
238 145         150         155         160
241 Pro Leu Ala Val Ile Gly Gly Gly Asp Ser Ala Met Glu Glu Ala Asn
242          165         170         175
245 Phe Leu Thr Lys Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp
246          180         185         190
249 Ala Phe Arg Ala Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro
250          195         200         205
253 Lys Ile Asp Val Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp
254          210         215         220
257 Gly Glu Arg Asp Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr
258 225         230         235         240
261 Gly Asp Val Ser Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly
262          245         250         255
265 His Glu Pro Ala Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser
266          260         265         270
269 Asp Gly Tyr Val Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro
270          275         280         285

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```
273 Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala
274      290      295      300
277 Ile Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His
278 305      310      315      320
281 Tyr Leu Gln Glu Ile Gly Ser Gln Glu Gly Lys Ser Asp
282      325      330
```

VERIFICATION SUMMARY

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